RAW SEQUENCE LISTING
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Application Serial Number: ___10/088,594___

Source: ___PCT10___

Date Processed by STIC: ___3|28|02___

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Revised 01/29/2002

Does Not Comply   PCT10
Corrected Diskette Needed

Errors on pp.2+7

RAW SEQUENCE LISTING   DATE: 03/28/2002
PATENT APPLICATION: US/10/088,594   TIME: 10:30:26

Input Set : A:\EP.txt
Output Set: N:\CRF3\03282002\J088594.raw

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     3 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD
     5 <120> TITLE OF INVENTION: Novel Transaldolase
     7 <130> FILE REFERENCE: 11236WO1
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/088,594
C--> 10 <141> CURRENT FILING DATE: 2002-03-21
    12 <150> PRIOR APPLICATION NUMBER: JP 99/266548
    13 <151> PRIOR FILING DATE: 1999-09-21
    15 <160> NUMBER OF SEQ ID NOS: 3
    17 <170> SOFTWARE: PatentIn Ver. 2.0
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length should be 1080!

ERRORED SEQUENCES

A coding sequence is always a nucleic sequence. Thus, response can only be DNA or RNA.

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    19 <210> SEQ ID NO: 1
    20 <211> LENGTH: 360
    21 <212> TYPE: PRT
    22 <213> ORGANISM: Corynebacterium glutamicum ATCC31388
    24 <400> SEQUENCE: 1
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    27 Met Ser His Ile Asp Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu
    28   1               5                  10                  15
    30 gac gac ctc tcc cgc gag cgc att act tcc ggc aat ctc agc cag gtt   96
    31 Asp Asp Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val
    32              20                  25                  30
    34 att gag gaa aag tct gta gtc ggt gtc acc acc aac cca gct att ttc  144
    35 Ile Glu Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe
    36          35                  40                  45
    38 gca gca gca atg tcc aag ggc gat tcc tac gac gct cag atc gca gag  192
    39 Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu
    40          50                  55                  60
    42 ctc aag gcc gct ggc gca tct gtt gac cag gct gtt tac gcc atg agc  240
    43 Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser
    44  65                  70                  75                  80
    46 atc gac gat gtt cgc aat gct tgt gat ctg ttc acc ggc atc ttc gag  288
    47 Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu
    48                  85                  90                  95
    50 tcc tcc aac ggc tac gac ggc cgc gtg tcc atc gag gtt gac cca cgt  336
    51 Ser Ser Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg
    52              100                 105                 110
    54 atc tct gct gac cgc gac gca acc ctg gct cag gcc aag gag ctg tgg  384
    55 Ile Ser Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp
    56          115                 120                 125
    58 gca aag gtt gat cgt cca aac gtc atg atc aag atc cct gca acc cca  432
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RAW SEQUENCE LISTING   DATE: 03/28/2002
PATENT APPLICATION: US/10/088,594   TIME: 10:30:26

Input Set : A:\EP.txt
Output Set: N:\CRF3\03282002\J088594.raw

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 60     130                 135                 140
 62 ggt tct ttg cca gca atc acc gac gct ttg gct gag ggc atc agc gtt    480
 63 Gly Ser Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val
 64 145                 150                 155                 160
 66 aac gtc acc ttg atc ttc tcc gtt gct cgc tac cgc gag gtc atc gct    528
 67 Asn Val Thr Leu Ile Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala
 68                 165                 170                 175
 70 gcg tac atc gag gga atc aag cag gca gct gca aac ggc cac gac gta    576
 71 Ala Tyr Ile Glu Gly Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val
 72                 180                 185                 190
 74 tcc aag atc cac tct gtg gct tcc ttc ttc gtc tcc cgc gtc gac gtt    624
 75 Ser Lys Ile His Ser Val Ala Ser Phe Phe Val Ser Arg Val Asp Val
 76             195                 200                 205
 78 gag atc gac aag cgc ctc gag gca atc gga tcc gat gag gct ttg gct    672
 79 Glu Ile Asp Lys Arg Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala
 80     210                 215                 220
 82 ctg cgc ggc aag gca ggc gtt gcc aac gct cag cgc gct tac gct gtg    720
 83 Leu Arg Gly Lys Ala Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val
 84 225                 230                 235                 240
 86 tac aag gag ctt ttc gac gcc gcc gag ctg cct gaa ggt gcc aac act    768
 87 Tyr Lys Glu Leu Phe Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr
 88                 245                 250                 255
 90 cag cgc cca ctg tgg gca tcc acc ggc gtg aag aac cct gcg tac gct    816
 91 Gln Arg Pro Leu Trp Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala
 92             260                 265                 270
 94 gca act ctt tac gtt tcc gag ctg gct ggt cca aac acc gtc aac acc    864
 95 Ala Thr Leu Tyr Val Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr
 96             275                 280                 285
 98 atg cca gaa ggc acc atc gac gct gtt ctg gaa ctg ggc aac ctg cac    912
 99 Met Pro Glu Gly Thr Ile Asp Ala Val Leu Glu Leu Gly Asn Leu His
100     290                 295                 300
102 ggt gac acc ctg tcc aac tcc gcg gca gaa gct gac gct gtg ttc tcc    960
103 Gly Asp Thr Leu Ser Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser
104 305                 310                 315                 320
106 cag ctt gag gct ctg ggc gtt gac ttg gca gat gtc ttc cag gtc ctg   1008
107 Gln Leu Glu Ala Leu Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu
108                 325                 330                 335
110 gag acc gag ggt gtg gac aag ttt gtt gct tct tgg agc gaa ctg ctt   1056
111 Glu Thr Glu Gly Val Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu
112             340                 345                 350
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E--> 114 gag tcc atg gaa gct cgc ctg aag ─────────────────────────→ 1080 !
E--> 115 Glu Ser Met Glu Ala Arg Leu Lys
E--> 116 <355⟩   360 ── number misaligned

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162 <210> SEQ ID NO: 3
163 <211> LENGTH: 4108
164 <212> TYPE: DNA
165 <213> ORGANISM: Corynebacterium glutamicum ATCC31388
167 <221> NAME/KEY: CDS
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170 <221> NAME/KEY: CDS
171 <222> LOCATION: (2643)..(3722)
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176 ttgcaccgta ttgcttgccg aacattttc ttttcctttc ggtttttcga gaattttcac 120
178 ctacaaaagc ccacgtcaca gctcccagac ttaagattgg tcacaccttt gacacatttg 180
180 aaccacagtt ggttataaaa tgggttcaac atcactatgg ttagaggtgt tgacgggtca 240
182 gattaagcaa agactacttt cggggtagat cacctttgcc aaatttgaat caattaacct 300
184 aagtcgtaga tctgatcatc ggatctaacg aaaacgaacc aaaactttgg tcccggttta 360
186 acccaggaag ga atg acc acc ttg acg ctg tca cct gaa ctt cag gcg ctc 411
187                Met Thr Thr Leu Thr Leu Ser Pro Glu Leu Gln Ala Leu
188                 1               5                  10
190 act gta cgc aat tac ccc tct gat tgg tcc gat gtg gac acc aag gct  459
191 Thr Val Arg Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala
192      15               20                  25
194 gta gac act gtt cgt gtc ctc gct gca gac gct gta gaa aac tgt ggc  507
195 Val Asp Thr Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly
196   30               35                  40                  45
198 tcc ggc cac cca ggc acc gca atg agc ctg gct ccc ctt gca tac acc  555
199 Ser Gly His Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr
200                 50                  55                  60
202 ttg tac cag cgg gtt atg aac gta gat cca cag gac acc aac tgg gca  603
203 Leu Tyr Gln Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala
204              65                  70                  75
206 ggc cgt gac cgc ttc gtt ctt tct tgt ggc cac tcc tct ttg acc cag  651
207 Gly Arg Asp Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln
208              80                  85                  90
210 tac atc cag ctt tac ttg ggt gga ttc ggc ctt gag atg gat gac ctg  699
211 Tyr Ile Gln Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu
212      95               100                 105
214 aag gct ctg cgc acc tgg gat tcc ttg acc cca gga cac cct gag tac  747
215 Lys Ala Leu Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr
216 110              115                 120                 125
218 cgc cac acc aag ggc gtt gag atc acc act ggc cct ctt ggc cag ggt  795
219 Arg His Thr Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly
220              130                 135                 140
222 ctt gca tct gca gtt ggt atg gcc atg gct gct cgt cgt gag cgt ggc  843
223 Leu Ala Ser Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly
224              145                 150                 155
226 cta ttc gac cca acc gct gct gag ggc gaa tcc cca ttc gac cac cac  891
227 Leu Phe Asp Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His
228              160                 165                 170
230 atc tac gtc att gct tct gat ggt gac ctg cag gaa ggt gtc acc tct  939
231 Ile Tyr Val Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser
232      175              180                 185
234 gag gca tcc tcc atc gct ggc acc cag cag ctg ggc aac ctc atc gtg  987
235 Glu Ala Ser Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val
236 190              195                 200                 205
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Input Set : A:\EP.txt
Output Set: N:\CRF3\03282002\J088594.raw


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238 ttc tgg gat gac aac cgc atc tcc atc gaa gac aac act gag atc gct   1035
239 Phe Trp Asp Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala
240                 210                 215                 220
242 ttc aac gag gac gtt gtt gct cgt tac aag gct tac ggc tgg cag acc   1083
243 Phe Asn Glu Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr
244                 225                 230                 235
246 att gag gtt gag gct ggc gag gac gtt gca gca atc gaa gct gca gtg   1131
247 Ile Glu Val Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val
248                 240                 245                 250
250 gct gag gct aag aag gac acc aag cga cct acc ttc atc cgc gtt cgc   1179
251 Ala Glu Ala Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg
252     255                 260                 265
254 acc atc atc ggc ttc cca gct cca acc atg atg aac acc ggt gct gtg   1227
255 Thr Ile Ile Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val
256 270                 275                 280                 285
258 cac ggt gct gct ctt ggc gca gct gag gtt gca gca acc aag act gag   1275
259 His Gly Ala Ala Leu Gly Ala Ala Glu Val Ala Ala Thr Lys Thr Glu
260                 290                 295                 300
262 ctt gga ttc gat cct gag gct cac ttc gcg atc gac gat gag gtt atc   1323
263 Leu Gly Phe Asp Pro Glu Ala His Phe Ala Ile Asp Asp Glu Val Ile
264                 305                 310                 315
266 gct cac acc cgc tcc ctc gca gag cgc gct gca cag aag aag gct gca   1371
267 Ala His Thr Arg Ser Leu Ala Glu Arg Ala Ala Gln Lys Lys Ala Ala
268                 320                 325                 330
270 tgg cag gtc aag ttc gat gag tgg gca gct gcc aac cct gag aac aag   1419
271 Trp Gln Val Lys Phe Asp Glu Trp Ala Ala Ala Asn Pro Glu Asn Lys
272     335                 340                 345
274 gct ctg ttc gat cgc ctg aac tcc cgt gag ctt cca gcg ggc tac gct   1467
275 Ala Leu Phe Asp Arg Leu Asn Ser Arg Glu Leu Pro Ala Gly Tyr Ala
276 350                 355                 360                 365
278 gac gag ctc cca aca tgg gat gca gat gag aag ggc gtc gca act cgt   1515
279 Asp Glu Leu Pro Thr Trp Asp Ala Asp Glu Lys Gly Val Ala Thr Arg
280                 370                 375                 380
282 aag gct tcc gag gct gca ctt cag gca ctg ggc aag acc ctt cct gag   1563
283 Lys Ala Ser Glu Ala Ala Leu Gln Ala Leu Gly Lys Thr Leu Pro Glu
284                 385                 390                 395
286 ctg tgg ggc ggt tcc gct gac ctc gca ggt tcc aac aac acc gtg atc   1611
287 Leu Trp Gly Gly Ser Ala Asp Leu Ala Gly Ser Asn Asn Thr Val Ile
288                 400                 405                 410
290 aag ggc tcc cct tcc ttc ggc cct gag tcc atc tcc acc gag acc tgg   1659
291 Lys Gly Ser Pro Ser Phe Gly Pro Glu Ser Ile Ser Thr Glu Thr Trp
292     415                 420                 425
294 tct gct gag cct tac ggc cgt aac ctg cac ttc ggt atc cgt gag cac   1707
295 Ser Ala Glu Pro Tyr Gly Arg Asn Leu His Phe Gly Ile Arg Glu His
296 430                 435                 440                 445
298 gct atg gga tcc atc ctc aac ggc att tcc ctc cac ggt ggc acc cgc   1755
299 Ala Met Gly Ser Ile Leu Asn Gly Ile Ser Leu His Gly Gly Thr Arg
300                 450                 455                 460
302 cca tac ggt gga acc ttc ctc atc ttc tcc gac tac atg cgt cct gca   1803
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303 Pro Tyr Gly Gly Thr Phe Leu Ile Phe Ser Asp Tyr Met Arg Pro Ala
304          465                 470                 475
306 gtt cgt ctt gca gct ctc atg gag acc gac gct tac tac gtc tgg acc  1851
307 Val Arg Leu Ala Ala Leu Met Glu Thr Asp Ala Tyr Tyr Val Trp Thr
308          480                 485                 490
310 cac gac tcc atc ggt ctg ggc gaa gat ggc cca acc cac cag cct gtt  1899
311 His Asp Ser Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val
312          495                 500                 505
314 gaa acc ttg gct gcg ctg cgc gcc atc cca ggt ctg tcc gtc ctg cgt  1947
315 Glu Thr Leu Ala Ala Leu Arg Ala Ile Pro Gly Leu Ser Val Leu Arg
316 510                 515                 520                 525
318 cct gca gat gcg aat gag acc gcc cag gct tgg gct gca gca ctt gag  1995
319 Pro Ala Asp Ala Asn Glu Thr Ala Gln Ala Trp Ala Ala Ala Leu Glu
320                  530                 535                 540
322 tac aag gaa ggc cct aag ggt ctt gca ctg acc cgc cag aac gtt cct  2043
323 Tyr Lys Glu Gly Pro Lys Gly Leu Ala Leu Thr Arg Gln Asn Val Pro
324                  545                 550                 555
326 gtt ctg gaa ggc acc aag gag aag gct gct gaa ggc gtt cgc cgc ggt  2091
327 Val Leu Glu Gly Thr Lys Glu Lys Ala Ala Glu Gly Val Arg Arg Gly
328          560                 565                 570
330 ggc tac gtc ctg gtt gag ggt tcc aag gaa acc cca gat gtg atc ctc  2139
331 Gly Tyr Val Leu Val Glu Gly Ser Lys Glu Thr Pro Asp Val Ile Leu
332          575                 580                 585
334 atg ggc tcc ggc tcc gag gtt cag ctt gca gtt aac gct gcg aaa gct  2187
335 Met Gly Ser Gly Ser Glu Val Gln Leu Ala Val Asn Ala Ala Lys Ala
336 590                 595                 600                 605
338 ctg gaa gct gag ggc gtt gca gct cgc gtt gtt tca gtt cct tgc atg  2235
339 Leu Glu Ala Glu Gly Val Ala Ala Arg Val Val Ser Val Pro Cys Met
340                  610                 615                 620
342 gat tgg ttc cag gag cag gac gca gag tac atc gag tcc gtt ctg cct  2283
343 Asp Trp Phe Gln Glu Gln Asp Ala Glu Tyr Ile Glu Ser Val Leu Pro
344                  625                 630                 635
346 gca gct gtg acc gct cgt gtg tct gtt gaa gct ggc atc gca atg cct  2331
347 Ala Ala Val Thr Ala Arg Val Ser Val Glu Ala Gly Ile Ala Met Pro
348          640                 645                 650
350 tgg tac cgc ttc ttg ggc acc cag ggc cgt gct gtc tcc ctt gag cac  2379
351 Trp Tyr Arg Phe Leu Gly Thr Gln Gly Arg Ala Val Ser Leu Glu His
352          655                 660                 665
354 ttc ggt gct tct gcg gat tac cag acc ctg ttt gag aag ttc ggc atc  2427
355 Phe Gly Ala Ser Ala Asp Tyr Gln Thr Leu Phe Glu Lys Phe Gly Ile
356 670                 675                 680                 685
358 acc acc gat gca gtc gtg gca gcg gcc aag gac tcc att aac agt      2472
359 Thr Thr Asp Ala Val Val Ala Ala Ala Lys Asp Ser Ile Asn Ser
360                  690                 695                 700
362 taattgccct gctgtttta gcttcaaccc ggggcagtat gattctccgg aattttattg 2532
364 ccccgggttg ttgttgttaa tcggtacaaa gggtcttaag cacatccctt acttgcctgc 2592
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367                                                            Met Ser
W--> 368                                                          1
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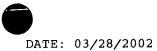
OK!

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       369 cac att gat gat ctt gca cag ctc ggc act tcc act tgg ctc gac gac   2696
       370 His Ile Asp Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu Asp Asp
W--> 371       5                   10                  15
       373 ctc tcc cgc gag cgc att act tcc ggc aat ctc agc cag gtt att gag   2744
       374 Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val Ile Glu
W--> 375       20                  25                  30
       377 gaa aag tct gta gtc ggt gtc acc acc aac cca gct att ttc gca gca   2792
       378 Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe Ala Ala
W--> 379 35                  40                  45                  50
       381 gca atg tcc aag ggc gat tcc tac gac gct cag atc gca gag ctc aag   2840
       382 Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu Leu Lys
W--> 383               55                  60                  65
       385 gcc gct ggc gca tct gtt gac cag gct gtt tac gcc atg agc atc gac   2888
       386 Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser Ile Asp
W--> 387               70                  75                  80
       389 gat gtt cgc aat gct tgt gat ctg ttc acc ggc atc ttc gag tcc tcc   2936
       390 Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu Ser Ser
W--> 391               85                  90                  95
       393 aac ggc tac gac ggc cgc gtg tcc atc gag gtt gac cca cgt atc tct   2984
       394 Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg Ile Ser
W--> 395       100                 105                 110
       397 gct gac cgc gac gca acc ctg gct cag gcc aag gag ctg tgg gca aag   3032
       398 Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp Ala Lys
W--> 399 115                 120                 125                 130
       401 gtt gat cgt cca aac gtc atg atc aag atc cct gca acc cca ggt tct   3080
       402 Val Asp Arg Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro Gly Ser
W--> 403               135                 140                 145
       405 ttg cca gca atc acc gac gct ttg gct gag ggc atc agc gtt aac gtc   3128
       406 Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val Asn Val
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       409 acc ttg atc ttc tcc gtt gct cgc tac cgc gag gtc atc gct gcg tac   3176
       410 Thr Leu Ile Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala Ala Tyr
W--> 411       165                 170                 175
       413 atc gag gga atc aag cag gca gct gca aac ggc cac gac gta tcc aag   3224
       414 Ile Glu Gly Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val Ser Lys
W--> 415       180                 185                 190
       417 atc cac tct gtg gct tcc ttc ttc gtc tcc cgc gtc gac gtt gag atc   3272
       418 Ile His Ser Val Ala Ser Phe Phe Val Ser Arg Val Asp Val Glu Ile
W--> 419 195                 200                 205                 210
       421 gac aag cgc ctc gag gca atc gga tcc gat gag gct ttg gct ctg cgc   3320
       422 Asp Lys Arg Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala Leu Arg
W--> 423               215                 220                 225
       425 ggc aag gca ggc gtt gcc aac gct cag cgc gct tac gct gtg tac aag   3368
       426 Gly Lys Ala Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val Tyr Lys
W--> 427               230                 235                 240
       429 gag ctt ttc gac gcc gcc gag ctg cct gaa ggt gcc aac act cag cgc   3416
       430 Glu Leu Phe Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr Gln Arg
W--> 431               245                 250                 255
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/088,594

Input Set : A:\EP.txt
Output Set: N:\CRF3\03282002\J088594.raw

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W--> 435       260                 265                 270
        437 ctt tac gtt tcc gag ctg gct ggt cca aac acc gtc aac acc atg cca   3512
        438 Leu Tyr Val Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr Met Pro
W--> 439 275                 280                 285                 290
        441 gaa ggc acc atc gac gct gtt ctg gaa ctg ggc aac ctg cac ggt gac   3560
        442 Glu Gly Thr Ile Asp Ala Val Leu Glu Leu Gly Asn Leu His Gly Asp
W--> 443                 295                 300                 305
        445 acc ctg tcc aac tcc gcg gca gaa gct gac gct gtg ttc tcc cag ctt   3608
        446 Thr Leu Ser Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser Gln Leu
W--> 447                 310                 315                 320
        449 gag gct ctg ggc gtt gac ttg gca gat gtc ttc cag gtc ctg gag acc   3656
        450 Glu Ala Leu Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu Glu Thr
W--> 451         325                 330                 335
        453 gag ggt gtg gac aag ttt gtt gct tct tgg agc gaa ctg ctt gag tcc   3704
        454 Glu Gly Val Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu Glu Ser
W--> 455         340                 345                 350
        457 atg gaa gct cgc ctg aag tagaatcagc acgctgcatc agtaacggcg          3752
        458 Met Glu Ala Arg Leu Lys
W--> 459 355                 360
        461 acatgaaatc gaattagttc gatcttatgt ggccgttaca catctttcat taaagaaagg 3812
        463 atcgtgacgc taccatcgtg agcacaaaca cgacccccgtc cagctggaca aacccactgc 3872
        465 gcgacccgca ggataaacga ctcccccgca tcgctggccc ttccggcatg gtgatcttcg 3932
        467 gtgtcactgg cgacttggct cgaaggaagc tgctcccgcg catttatgat ctagcaaacc 3992
        469 gcggattgct gcccccagga ttctcgttgg taggttacgg ccgccgcgaa tggtccaaag 4052
        471 aagactttga aaaatacgta cgcgatgccg caagtgctgg tgctcgtacg gaattc       4108
E--> 476 10/12  —delete
```

VERIFICATION SUMMARY   DATE: 03/28/2002
PATENT APPLICATION: **US/10/088,594**   TIME: 10:30:27

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\03282002\J088594.raw**

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:114 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
L:115 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=1
L:116 M:252 E: No. of Seq. differs, <211>LENGTH:Input:360 Found:368 SEQ:1
L:368 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:371 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:375 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:379 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:383 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:387 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:391 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:395 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:399 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:403 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:407 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:411 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:415 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:419 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:423 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:427 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:431 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:435 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:439 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:443 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:447 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:451 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:455 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:459 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:476 M:254 E: No. of Bases conflict, LENGTH:Input:12 Counted:4109 SEQ:3
L:476 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:476 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4108 Found:4109 SEQ:3